

REMARKS

I. Substitute Specification

A substitute specification is provided under 37 CFR 1.125(a) as requested.

Applicants request that pages 1-100 of the specification as filed be replaced with pages 1-83 of the enclosed substitute specification. As discussed with the Examiner, the claims will remain as currently pending following entry of the amendment filed April 30, 2004, and the Examiner has requested that the claims not be included in the substitute specification. A marked up version of the substitute specification to show the changes made is also enclosed.

The changes in general include those amendments made in the preliminary amendments filed August 16, 2001, which have not been entered. The "Description of the Figures" section has also been amended so the figure references correspond to the amended figure legends of some of the replacement drawings (see below). The priority section of the application has been amended to delete the priority claim to U.S. Application No. 08/724,643, filed October 1, 1996. The Accession number for lambda clone 25-1.1 (No. 209024) that was not available at the time the priority application was filed has also been inserted at page 16, line 56-57 and page 82, line 10 of the substitute specification. A copy of the deposit letter is enclosed.

None of the amendments introduce new matter. The substitute specification that is provided thus introduces no new matter.

II. Formal Drawings

A complete set of formal drawings are attached. The figure references for FIGS. 9, 12, 30, 42, 46, 47, 50, 51 and 53 that each include multiple sheets have been amended so the additional sheets no longer say "continued" but instead are labeled as sheets "A", "B," "C", etc.

Applicants also submit a correction to Figure 53. Figure 53 shows the DNA sequence of plasmid pGRN121, and the polypeptide encoded by this sequence (see the original specification at, e.g., page 99, lines 14-17, and page 19, lines 16-17). Applicants sequenced plasmid pGRN121, which was deposited with the American Type Culture Collection as ATCC

accession #209016 on May 6, 1997, prior to the filing of the subject application. The deposit is noted in the original specification at page 98, lines 12-21. Although Applicants correctly determined the protein coding sequence of pGRN121, three nucleotide errors of an editorial or typographical nature were introduced during the preparation of the documents used as the basis for Figure 53. As noted in the accompanying annotated sheets, the codon at position 578 was transcribed as "CCG (pro)" and has been corrected to "AAG (lys)," and the codon at position 958 was transcribed as "GTC (val)" and has been corrected to "CTC (leu)." The coding sequence of pGRN121 is an inherent property of the deposited plasmid, providing basis for this correction, and there is no new matter added by this correction.

The sequence listing submitted August 16, 2001 provides the nucleotide and amino acid sequences as shown in the corrected version of Figure 53. Thus, no changes to the sequence listing are required.

Although Applicants do not believe that any additional fee is due as part of this submission, if an additional fee is due, the Examiner is authorized to charge such fee to Deposit Account 20-1430.

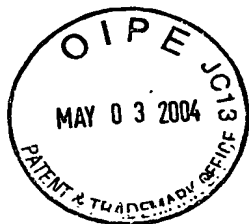
If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 303-571-4000.

Respectfully submitted,



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Attachments
SLA:sla
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430
ala ala gly val cys ala arg glu lys pro gln gly ser val ala
GCA GCC GGT GTC TGT GCC CGG GAG AAG CCC CAG GGC TCT GTG GCG

440
ala pro glu glu glu asp thr asp pro arg arg leu val gln leu
GCC CCC GAG GAG GAG GAC ACA GAC CCC CGT CGC CTG GTG CAG CTG

450
leu arg gln his ser ser pro trp gln val tyr gly phe val arg
CTC CGC CAG CAC AGC AGC CCC TGG CAG GTG TAC GGC TTC GTG CCG

460
ala cys leu arg arg leu val pro pro gly leu trp gly ser arg
GCC TGC CTG CGC CGG CTG GTG CCC CCA GGC CTC TGG GGC TCC AGG

470
his asn glu arg arg phe leu arg asn thr lys lys phe ile ser
CAC AAC GAA CGC CGC TTC CTC AGG AAC ACC AAG AAG TTC ATC TCC

480
leu gly lys his ala lys leu ser leu gln glu leu thr trp lys
CTG GGG AAG CAT GCC AAG CTC TCG CTG CAG GAG CTG ACG TGG AAG

490
met ser val arg asp cys ala trp leu arg arg ser pro gly val
ATG AGC GTG CGG GAC TGC GCT TGG CTG CGC AGG AGC CCA GGG GTT

500
gly cys val pro ala ala glu his arg leu arg glu glu ile leu
GGC TGT GTT CCG GCC GCA GAG CAC CGT CTG CGT GAG GAG ATC CTG

510
ala lys phe leu his trp leu met ser val tyr val val glu leu
GCC AAG TTC CTG CAC TGG CTG ATG AGT GTG TAC GTC GTC GAG CTG

520
leu arg ser phe phe tyr val thr glu thr thr phe gln lys asn
CTC AGG TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC

530
arg leu phe phe tyr arg ^{lys} pro ser val trp ser lys leu gln ser
AGG CTC TTT TTC TAC CGG CCG AGT GTC TGG AGC AAG TTG CAA AGC

540
ile gly ile arg gln his leu lys arg val gln leu arg glu leu
ATT GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG

550
ser glu ala glu val arg gln his arg glu ala arg pro ala leu
TCG GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG

560
leu thr ser arg leu arg phe ile pro lys pro asp gly leu arg
CTG ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CCG

570
pro ile val asn met asp tyr val val gly ala arg thr phe arg
CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC

580
pro ile val asn met asp tyr val val gly ala arg thr phe arg
CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC

590
ile gly ile arg gln his leu lys arg val gln leu arg glu leu
ATT GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG

600
ser glu ala glu val arg gln his arg glu ala arg pro ala leu
TCG GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG

610
leu thr ser arg leu arg phe ile pro lys pro asp gly leu arg
CTG ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CCG

620
pro ile val asn met asp tyr val val gly ala arg thr phe arg
CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC

630
pro ile val asn met asp tyr val val gly ala arg thr phe arg
CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC

640
pro ile val asn met asp tyr val val gly ala arg thr phe arg
CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC

FIG. 53C



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880
leu val thr pro his leu thr his ala lys thr phe leu arg thr
TTG GTG ACA CCT CAC CTC ACC CAC GCG AAA ACC TTC CTC AGG ACC

890
leu val arg gly val pro glu tyr gly cys val val asn leu arg
CTG GTC CGA GGT GTC CCT GAG TAT GGC TGC GTG GTG AAC TTG CGG

910
lys thr val val asn phe pro val glu asp glu ala leu gly gly
AAG ACA GTG GTG AAC TTC CCT GTA GAA GAC GAG GCC CTG GGT GGC

920
thr ala phe val gln met pro ala his gly leu phe pro trp cys
ACG GCT TTT GTT CAG ATG CCG GCC CAC GGC CTA TTC CCC TGG TGC

940
gly leu leu leu asp thr arg thr leu glu val gln ser asp tyr
GGC CTG CTG CTG GAT ACC CGG ACC CTG GAG GTG CAG AGC GAC TAC

950
ser ser tyr ala arg thr ser ile arg ala ser leuval thr phe asn
TCC AGC TAT GCC CGG ACC TCC ATC AGA GCC AGT GTC ACC TTC AAC

960
arg gly phe lys ala gly arg asn met arg arg lys leu phe gly
CGC GGC TTC AAG GCT GGG AGG AAC ATG CGT CGC AAA CTC TTT GGG

970
val leu arg leu lys cys his ser leu phe leu asp leu gln val
GTC TTG CGG CTG AAG TGT CAC AGC CTG TTT CTG GAT TTG CAG GTG

980
asn ser leu gln thr val cys thr asn ile tyr lys ile leu leu
AAC AGC CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG

1000
leu gln ala tyr arg phe his ala cys val leu gln leu pro phe
CTG CAG GCG TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT

1010
his gln gln val trp lys asn pro thr phe phe leu arg val ile
CAT CAG CAA GTT TGG AAG AAC CCC ACA TTT TTC CTG CGC GTC ATC

1020
ser asp thr ala ser leu cys tyr ser ile leu lys ala lys asn
TCT GAC ACG GCC TCC CTC TGC TAC TCC ATC CTG AAA GCC AAG AAC

1030
ala gly met ser leu gly ala lys gly ala ala gly pro leu pro
GCA GGG ATG TCG CTG GGG GCC AAG GGC GCC GCC GGC CCT CTG CCC

1040
ser glu ala val gln trp leu cys his gln ala phe leu leu lys
TCC GAG GCC GTG CAG TGG CTG TGC CAC CAA GCA TTC CTG CTC AAG

1050
leu thr arg his arg val thr tyr val pro leu leu gly ser leu
CTG ACT CGA CAC CGT GTC ACC TAC GTG CCA CTC CTG GGG TCA CTC

1060
1070
1080
1090

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FIG. 53E